

SEQUENCE LISTING



<110> Freyssinet, Georges
Rang, Cecile
Frutos, Roger

<120> Pepsin-sensitive modified *Bacillus thuringiensis* insecticidal toxin

<130> A35992-PCT-USA-A (072667.0191)

<140> 10/665,460

<141> 2003-09-19

<150> PCT/FR02/00772

<151> 2002-03-04

<150> FR 01/03691

<151> 2001-03-19

<160> 160

<170> PatentIn Ver. 2.1

<210> 1

<211> 2019

<212> DNA

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<222> (1)..(2019)

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Val	Arg	Leu	Gly	Ser	Thr	Met	Asn	Arg	Gly	Gln	Glu	Leu	Thr	Tyr	Glu	
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Ser	Phe	Phe	Thr	Arg	Glu	Phe	Thr	Thr	Thr	Gly	Pro	Phe	Asn	Pro	Pro	
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Asn Asp Thr Leu Asn Leu Ser Val Val Arg Ala Gln Phe Ile Ala Leu
165 170 175

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225					230					235					240		
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Asp	Arg		
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Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe		
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Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly		
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Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser		
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Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	Ser	Phe		
465					470					475					480		

Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr	
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Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	Thr	Pro	
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Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro	Val	Ser	
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Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr	Val	Asn	
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Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Val	Arg	Phe	Ala	Ser	Thr	
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Ser	Phe	Phe	Thr	Arg	Glu	Phe	Thr	Thr	Thr	Gly	Pro	Phe	Asn	Pro	Pro	
	610					615					620					
Phe	Thr	Phe	Thr	Gln	Ala	Gln	Glu	Ile	Leu	Thr	Val	Asn	Ala	Glu	Gly	
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Val	Ser	Thr	Gly	Gly	Glu	Tyr	Tyr	Ile	Asp	Arg	Ile	Glu	Ile	Val	Pro	
				645					650					655		
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 <211> 2019
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description: Cry9Ca1 Phe-164

<220>
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Cys	Gly	Cys	Pro	Ser	Asp	Asp	Asp	Val	Arg	Tyr	Pro	Leu	Ala	Ser	Asp	
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cca	aat	gca	gcg	tta	caa	aat	atg	aac	tat	aaa	gat	tac	tta	caa	atg	144
Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met	
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aca	gat	gag	gac	tac	act	gat	tct	tat	ata	aat	cct	agt	tta	tct	att	192
Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile	
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Ser	Gly	Arg	Asp	Ala	Val	Gln	Thr	Ala	Leu	Thr	Val	Val	Gly	Arg	Ile	
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Leu	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ser	Gly	Gln	Ile	Val	Ser	Phe	Tyr	
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caa	ttc	ctt	tta	aat	aca	ctg	tgg	cca	gtt	aat	gat	aca	gct	ata	tgg	336
Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp	
			100					105					110			
gaa	gct	ttc	atg	cga	cag	gtg	gag	gaa	ctt	gtc	aat	caa	caa	ata	aca	384
Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr	
		115					120					125				
gaa	ttt	gca	aga	aat	cag	gca	ctt	gca	aga	ttg	caa	gga	tta	gga	gac	432
Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Asp	
	130					135					140					
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Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg	
	145				150					155					160	
aat	gat	aca	ttt	aat	tta	agt	gtt	gtt	cgt	gct	caa	ttt	ata	gct	tta	528
Asn	Asp	Thr	Phe	Asn	Leu	Ser	Val	Val	Arg	Ala	Gln	Phe	Ile	Ala	Leu	
				165					170					175		
gac	ctt	gat	ttt	gtt	aat	gct	att	cca	ttg	ttt	gca	gta	aat	gga	cag	576
Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln	
			180					185					190			
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Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Val	Asn	Leu	His	Leu	
		195					200					205				
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Leu	Leu	Leu	Lys	Asp	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr	
	210					215					220					
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Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Asp	Arg	Gln	Leu	Glu	Leu	Thr	Ala	
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Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Trp	Leu	Arg	Tyr	His	Gln	Phe	Arg	
			260					265					270			
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Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr	
		275					280					285				
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Tyr	Asp	Val	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg	
	290					295					300					
gag	gta	tat	aca	gat	ccg	att	gta	ttt	aat	cca	cca	gct	aat	ggt	gga	960
Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Val	Gly	
305					310					315					320	
ctt	tgc	cga	cgt	tgg	ggt	act	aat	ccc	tat	aat	act	ttt	tct	gag	ctc	1008
Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu	
				325					330					335		
gaa	aat	gcc	ttc	att	cgc	cca	cca	cat	ctt	ttt	gat	agg	ctg	aat	agc	1056
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Asp	Arg	Leu	Asn	Ser	
			340					345					350			
tta	aca	atc	agc	agt	aat	cga	ttt	cca	ggt	tca	tct	aat	ttt	atg	gat	1104
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Asp	
		355					360					365				
tat	tgg	tca	gga	cat	acg	tta	cgc	cgt	agt	tat	ctg	aac	gat	tca	gca	1152
Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala	
	370					375					380					
gta	caa	gaa	gat	agt	tat	ggc	cta	att	aca	acc	aca	aga	gca	aca	att	1200
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile	
385					390					395					400	
aat	ccc	gga	ggt	gat	gga	aca	aac	cgc	ata	gag	tca	acg	gca	gta	gat	1248
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp	
				405					410					415		
ttt	cgt	tct	gca	ttg	ata	ggc	ata	tat	ggc	gtg	aat	aga	gct	tct	ttt	1296
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe	
			420					425					430			
gtc	cca	gga	ggc	ttg	ttt	aat	ggc	acg	act	tct	cct	gct	aat	gga	gga	1344
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly	
		435					440					445				
tgt	aga	gat	ctc	tat	gat	aca	aat	gat	gaa	tta	cca	cca	gat	gaa	agt	1392
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser	
	450					455					460					
acc	gga	agt	tca	acc	cat	aga	cta	tct	cat	ggt	acc	ttt	ttt	agc	ttt	1440

Thr 465	Gly	Ser	Ser	Thr	His 470	Arg	Leu	Ser	His	Val 475	Thr	Phe	Phe	Ser	Phe 480	
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tat Tyr	gtt Val	tgg Trp	acc Thr 500	cgt Arg	cgt Arg	gat Asp	gtg Val	gac Asp 505	ctt Leu	aat Asn	aat Asn	acg Thr	att Ile 510	acc Thr	cca Pro	1536
aat Asn	aga Arg	att Ile 515	aca Thr	caa Gln	tta Leu	cca Pro	ttg Leu 520	gta Val	aag Lys	gca Ala	tct Ser	gca Ala 525	cct Pro	gtt Val	tcg Ser	1584
ggt Gly 530	act Thr	acg Thr	gtc Val	tta Leu	aaa Lys	ggt Gly 535	cca Pro	gga Gly	ttt Phe	aca Thr 540	gga Gly	ggg Gly	ggt Gly	ata Ile	ctc Leu	1632
cga Arg 545	aga Arg	aca Thr	act Thr	aat Asn	ggc Gly 550	aca Thr	ttt Phe	gga Gly	acg Thr	tta Leu 555	aga Arg	gta Val	acg Thr	gtt Val	aat Asn 560	1680
tca Ser	cca Pro	tta Leu	aca Thr 565	caa Gln	caa Gln	tat Tyr	cgc Arg	cta Leu	aga Arg 570	gtt Val	cgt Arg	ttt Phe	gcc Ala 575	tca Ser	aca Thr	1728
gga Gly	aat Asn	ttc Phe 580	agt Ser	ata Ile	agg Arg	gta Val	ctc Leu	cgt Arg 585	gga Gly	ggg Gly	gtt Val	tct Ser	atc Ile 590	ggt Gly	gat Asp	1776
gtt Val	aga Arg 595	tta Leu	ggg Gly	agc Ser	aca Thr	atg Met	aac Asn 600	aga Arg	ggg Gly	cag Gln	gaa Glu	cta Leu 605	act Thr	tac Tyr	gaa Glu	1824
tcc Ser 610	ttt Phe	ttc Phe	aca Thr	aga Arg	gag Glu	ttt Phe 615	act Thr	act Thr	act Thr	ggt Gly 620	ccg Pro	ttc Phe	aat Asn	ccg Pro	cct Pro	1872
ttt Phe 625	aca Thr	ttt Phe	aca Thr	caa Gln	gct Ala	caa Gln 630	gag Glu	att Ile	cta Leu	aca Thr 635	gtg Val	aat Asn	gca Ala	gaa Glu	ggt Gly 640	1920
gtt Val	agc Ser	acc Thr	ggt Gly	ggt Gly	gaa Glu	tat Tyr	tat Tyr	ata Ile	gat Asp 650	aga Arg	att Ile	gaa Glu	att Ile	gtc Val 655	cct Pro	1968
gtg Val	aat Asn	ccg Pro	gca Ala	cga Arg	gaa Glu	gcg Ala	gaa Glu	gag Glu	gat Asp	tta Leu	gaa Glu	gcg Ala	gcg Ala	aag Lys	aaa Lys	2016
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<211> 673

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial sequence description: Cry9Ca1 Phe-164

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			20					25					30			
Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met	
		35					40					45				
Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile	
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Ser	Gly	Arg	Asp	Ala	Val	Gln	Thr	Ala	Leu	Thr	Val	Val	Gly	Arg	Ile	
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Leu	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ser	Gly	Gln	Ile	Val	Ser	Phe	Tyr	
				85					90					95		
Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp	
			100					105					110			
Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr	
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Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Asp	
	130					135					140					
Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg	
145					150					155					160	
Asn	Asp	Thr	Phe	Asn	Leu	Ser	Val	Val	Arg	Ala	Gln	Phe	Ile	Ala	Leu	
				165					170					175		
Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln	
			180					185					190			
Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Val	Asn	Leu	His	Leu	
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Leu	Leu	Leu	Lys	Asp	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr	
	210					215					220					
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Asp	Arg	Gln	Leu	Glu	Leu	Thr	Ala	
225					230					235					240	
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Asp	Arg	
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Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Trp	Leu	Arg	Tyr	His	Gln	Phe	Arg	
			260					265					270			

Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr		
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Tyr	Asp	Val	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg		
	290					295					300						
Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Val	Gly		
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Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu		
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Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Asp	Arg	Leu	Asn	Ser		
			340					345					350				
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Asp		
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Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala		
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385					390					395					400		
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				405					410					415			
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe		
			420					425					430				
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly		
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Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser		
	450					455					460						
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	Ser	Phe		
465					470					475					480		
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr		
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Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	Thr	Pro		
			500					505					510				
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Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr	Val	Asn		
545					550					555					560		
Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Val	Arg	Phe	Ala	Ser	Thr		
				565					570					575			

Gly	Asn	Phe	Ser	Ile	Arg	Val	Leu	Arg	Gly	Gly	Val	Ser	Ile	Gly	Asp
			580					585					590		
Val	Arg	Leu	Gly	Ser	Thr	Met	Asn	Arg	Gly	Gln	Glu	Leu	Thr	Tyr	Glu
		595					600					605			
Ser	Phe	Phe	Thr	Arg	Glu	Phe	Thr	Thr	Thr	Gly	Pro	Phe	Asn	Pro	Pro
	610					615					620				
Phe	Thr	Phe	Thr	Gln	Ala	Gln	Glu	Ile	Leu	Thr	Val	Asn	Ala	Glu	Gly
625					630					635					640
Val	Ser	Thr	Gly	Gly	Glu	Tyr	Tyr	Ile	Asp	Arg	Ile	Glu	Ile	Val	Pro
			645						650					655	
Val	Asn	Pro	Ala	Arg	Glu	Ala	Glu	Glu	Asp	Leu	Glu	Ala	Ala	Lys	Lys
			660					665					670		

Ala

<210> 7
 <211> 2019
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description: Cry9Ca1 Glu-164

<220>
 <221> CDS
 <222> (1)..(2019)

<400> 7																
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Met	Asn	Arg	Asn	Asn	Gln	Asn	Glu	Tyr	Glu	Ile	Ile	Asp	Ala	Pro	His	
1				5				10					15			
tgt	ggg	tgt	cca	tca	gat	gac	gat	gtg	agg	tat	cct	ttg	gca	agt	gac	96
Cys	Gly	Cys	Pro	Ser	Asp	Asp	Asp	Val	Arg	Tyr	Pro	Leu	Ala	Ser	Asp	
			20					25					30			
cca	aat	gca	gcg	tta	caa	aat	atg	aac	tat	aaa	gat	tac	tta	caa	atg	144
Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met	
		35					40					45				
aca	gat	gag	gac	tac	act	gat	tct	tat	ata	aat	cct	agt	tta	tct	att	192
Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile	
	50					55					60					
agt	ggt	aga	gat	gca	gtt	cag	act	gcg	ctt	act	gtt	gtt	ggg	aga	ata	240
Ser	Gly	Arg	Asp	Ala	Val	Gln	Thr	Ala	Leu	Thr	Val	Val	Gly	Arg	Ile	
65					70				75						80	

ctc ggg gct tta ggt gtt ccg ttt tct gga caa ata gtg agt ttt tat	288
Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser Phe Tyr	
85 90 95	
caa ttc ctt tta aat aca ctg tgg cca gtt aat gat aca gct ata tgg	336
Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala Ile Trp	
100 105 110	
gaa gct ttc atg cga cag gtg gag gaa ctt gtc aat caa caa ata aca	384
Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln Ile Thr	
115 120 125	
gaa ttt gca aga aat cag gca ctt gca aga ttg caa gga tta gga gac	432
Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Asp	
130 135 140	
tct ttt aat gta tat caa cgt tcc ctt caa aat tgg ttg gct gat cga	480
Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg	
145 150 155 160	
aat gat aca gaa aat tta agt gtt gtt cgt gct caa ttt ata gct tta	528
Asn Asp Thr Glu Asn Leu Ser Val Val Arg Ala Gln Phe Ile Ala Leu	
165 170 175	
gac ctt gat ttt gtt aat gct att cca ttg ttt gca gta aat gga cag	576
Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln	
180 185 190	
cag gtt cca tta ctg tca gta tat gca caa gct gtg aat tta cat ttg	624
Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Val Asn Leu His Leu	
195 200 205	
tta tta tta aaa gat gca tct ctt ttt gga gaa gga tgg gga ttc aca	672
Leu Leu Leu Lys Asp Ala Ser Leu Phe Gly Glu Gly Trp Gly Phe Thr	
210 215 220	
cag ggg gaa att tcc aca tat tat gac cgt caa ttg gaa cta acc gct	720
Gln Gly Glu Ile Ser Thr Tyr Tyr Asp Arg Gln Leu Glu Leu Thr Ala	
225 230 235 240	
aag tac act aat tac tgt gaa act tgg tat aat aca ggt tta gat cgt	768
Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu Asp Arg	
245 250 255	
tta aga gga aca aat act gaa agt tgg tta aga tat cat caa ttc cgt	816
Leu Arg Gly Thr Asn Thr Glu Ser Trp Leu Arg Tyr His Gln Phe Arg	
260 265 270	
aga gaa atg act tta gtg gta tta gat gtt gtg gcg cta ttt cca tat	864
Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe Pro Tyr	
275 280 285	
tat gat gta cga ctt tat cca acg gga tca aac cca cag ctt aca cgt	912
Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg	
290 295 300	
gag gta tat aca gat ccg att gta ttt aat cca cca gct aat gtt gga	960

Glu 305	Val	Tyr	Thr	Asp	Pro 310	Ile	Val	Phe	Asn	Pro 315	Pro	Ala	Asn	Val	Gly 320	
ctt	tgc	cga	cgt	tgg	ggg	act	aat	ccc	tat	aat	act	ttt	tct	gag	ctc	1008
Leu	Cys	Arg	Arg	Trp	Gly 325	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu	
gaa	aat	gcc	ttc	att	cgc	cca	cca	cat	ctt	ttt	gat	agg	ctg	aat	agc	1056
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Asp	Arg	Leu	Asn	Ser	
tta	aca	atc	agc	agt	aat	cga	ttt	cca	gtt	tca	tct	aat	ttt	atg	gat	1104
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Asp	
tat	tgg	tca	gga	cat	acg	tta	cgc	cgt	agt	tat	ctg	aac	gat	tca	gca	1152
Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala	
gta	caa	gaa	gat	agt	tat	ggc	cta	att	aca	acc	aca	aga	gca	aca	att	1200
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile	
aat	ccc	gga	gtt	gat	gga	aca	aac	cgc	ata	gag	tca	acg	gca	gta	gat	1248
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp	
ttt	cgt	tct	gca	ttg	ata	ggg	ata	tat	ggc	gtg	aat	aga	gct	tct	ttt	1296
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe	
gtc	cca	gga	ggc	ttg	ttt	aat	ggg	acg	act	tct	cct	gct	aat	gga	gga	1344
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly	
tgt	aga	gat	ctc	tat	gat	aca	aat	gat	gaa	tta	cca	cca	gat	gaa	agt	1392
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser	
acc	gga	agt	tca	acc	cat	aga	cta	tct	cat	gtt	acc	ttt	ttt	agc	ttt	1440
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	Ser	Phe	
caa	act	aat	cag	gct	gga	tct	ata	gct	aat	gca	gga	agt	gta	cct	act	1488
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr	
tat	gtt	tgg	acc	cgt	cgt	gat	gtg	gac	ctt	aat	aat	acg	att	acc	cca	1536
Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	Thr	Pro	
aat	aga	att	aca	caa	tta	cca	ttg	gta	aag	gca	tct	gca	cct	gtt	tcg	1584
Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro	Val	Ser	
ggg	act	acg	gtc	tta	aaa	ggg	cca	gga	ttt	aca	gga	ggg	ggg	ata	ctc	1632
Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	Ile	Leu	

530	535	540	
cga aga aca act aat ggc aca ttt gga acg tta aga gta acg gtt aat			1680
Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn			
545	550	555	560
tca cca tta aca caa caa tat cgc cta aga gtt cgt ttt gcc tca aca			1728
Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Val Arg Phe Ala Ser Thr			
	565	570	575
gga aat ttc agt ata agg gta ctc cgt gga ggg gtt tct atc ggt gat			1776
Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp			
	580	585	590
gtt aga tta ggg agc aca atg aac aga ggg cag gaa cta act tac gaa			1824
Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu			
	595	600	605
tcc ttt ttc aca aga gag ttt act act act ggt ccg ttc aat ccg cct			1872
Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro			
	610	615	620
ttt aca ttt aca caa gct caa gag att cta aca gtg aat gca gaa ggt			1920
Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly			
625	630	635	640
gtt agc acc ggt ggt gaa tat tat ata gat aga att gaa att gtc cct			1968
Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro			
	645	650	655
gtg aat ccg gca cga gaa gcg gaa gag gat tta gaa gcg gcg aag aaa			2016
Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys			
	660	665	670
gcg			2019
Ala			

<210> 8

<211> 673

<212> PRT

<213> Artificial sequence

<220>

<223> Artificial sequence description: Cry9Ca1 Glu-164

<400> 8

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			20				25					30			

Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met
		35				40					45				

Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50					55					60					
Ser	Gly	Arg	Asp	Ala	Val	Gln	Thr	Ala	Leu	Thr	Val	Val	Gly	Arg	Ile
65					70					75					80
Leu	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ser	Gly	Gln	Ile	Val	Ser	Phe	Tyr
				85					90					95	
Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp
			100					105					110		
Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr
		115					120					125			
Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Asp
		130				135					140				
Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg
145					150					155					160
Asn	Asp	Thr	Glu	Asn	Leu	Ser	Val	Val	Arg	Ala	Gln	Phe	Ile	Ala	Leu
				165					170					175	
Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln
			180					185					190		
Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Val	Asn	Leu	His	Leu
		195					200					205			
Leu	Leu	Leu	Lys	Asp	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr
		210				215					220				
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Asp	Arg	Gln	Leu	Glu	Leu	Thr	Ala
225					230					235					240
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Asp	Arg
				245					250					255	
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Trp	Leu	Arg	Tyr	His	Gln	Phe	Arg
			260					265					270		
Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr
		275					280					285			
Tyr	Asp	Val	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg
	290					295					300				
Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Val	Gly
305					310					315					320
Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu
				325					330					335	
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Asp	Arg	Leu	Asn	Ser
			340					345					350		
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Asp

355	360	365															
Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala		
370						375					380						
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile		
385					390					395					400		
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp		
				405					410					415			
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe		
			420					425					430				
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly		
		435					440					445					
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser		
450						455					460						
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	Ser	Phe		
465					470					475					480		
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr		
				485					490					495			
Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	Thr	Pro		
			500					505					510				
Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro	Val	Ser		
		515					520					525					
Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	Ile	Leu		
530						535					540						
Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr	Val	Asn		
545					550					555					560		
Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Val	Arg	Phe	Ala	Ser	Thr		
				565					570					575			
Gly	Asn	Phe	Ser	Ile	Arg	Val	Leu	Arg	Gly	Gly	Val	Ser	Ile	Gly	Asp		
			580					585					590				
Val	Arg	Leu	Gly	Ser	Thr	Met	Asn	Arg	Gly	Gln	Glu	Leu	Thr	Tyr	Glu		
		595					600					605					
Ser	Phe	Phe	Thr	Arg	Glu	Phe	Thr	Thr	Thr	Gly	Pro	Phe	Asn	Pro	Pro		
610						615					620						
Phe	Thr	Phe	Thr	Gln	Ala	Gln	Glu	Ile	Leu	Thr	Val	Asn	Ala	Glu	Gly		
625					630					635					640		
Val	Ser	Thr	Gly	Gly	Glu	Tyr	Tyr	Ile	Asp	Arg	Ile	Glu	Ile	Val	Pro		
			645						650					655			
Val	Asn	Pro	Ala	Arg	Glu	Ala	Glu	Glu	Asp	Leu	Glu	Ala	Ala	Lys	Lys		

660

665

670

Ala

<210> 9

<211> 2019

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: Cry9Ca1-100%

<220>

<221> CDS

<222> (1)..(2019)

<400> 9

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tgt ggg tgt cca tca gaa gaa gaa tta agg tat cct ttg gca agt gaa	96
Cys Gly Cys Pro Ser Glu Glu Glu Leu Arg Tyr Pro Leu Ala Ser Glu	
20 25 30	
cca aat gca gcg tta caa aat atg aac tat aaa gaa tac tta caa atg	144
Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Glu Tyr Leu Gln Met	
35 40 45	
aca gaa gag gaa tac act gaa tct tat ata aat cct agt tta tct att	192
Thr Glu Glu Glu Tyr Thr Glu Ser Tyr Ile Asn Pro Ser Leu Ser Ile	
50 55 60	
agt ggt aga gaa gca tta cag act gcg ctt act gtt att agg aga ata	240
Ser Gly Arg Glu Ala Leu Gln Thr Ala Leu Thr Val Ile Arg Arg Ile	
65 70 75 80	
ctc ggg gct tta ggt tta ccg ttt tct gga caa ata tta agt ttt tat	288
Leu Gly Ala Leu Gly Leu Pro Phe Ser Gly Gln Ile Leu Ser Phe Tyr	
85 90 95	
caa ttc ctt tta aat aca ctg ttt cca tta aat gaa aca gct ata ttt	336
Gln Phe Leu Leu Asn Thr Leu Phe Pro Leu Asn Glu Thr Ala Ile Phe	
100 105 110	
gaa gct ttc atg cga cag tta gag gaa ctt tta aat caa caa ata aca	384
Glu Ala Phe Met Arg Gln Leu Glu Glu Leu Leu Asn Gln Gln Ile Thr	
115 120 125	
gaa ttt gca aga aat cag gca ctt gca aga ttg caa gga tta gga gaa	432
Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Glu	
130 135 140	
tct ttt aat tta tat caa cgt tcc ctt caa aat ttt ttg gct gaa cga	480

Ser 145	Phe	Asn	Leu	Tyr	Gln 150	Arg	Ser	Leu	Gln	Asn 155	Phe	Leu	Ala	Glu	Arg 160	
aat	gaa	aca	cga	aat	tta	agt	tta	tta	cgt	gct	caa	ttt	ata	gct	tta	528
Asn	Glu	Thr	Arg	Asn 165	Leu	Ser	Leu	Leu	Arg 170	Ala	Gln	Phe	Ile	Ala	Leu 175	
gaa	ctt	gaa	ttt	tta	aat	gct	att	cca	ttg	ttt	gca	tta	aat	gga	cag	576
Glu	Leu	Glu	Phe 180	Leu	Asn	Ala	Ile	Pro 185	Leu	Phe	Ala	Leu	Asn	Gly	Gln 190	
cag	tta	cca	tta	ctg	tca	tta	tat	gca	caa	gct	tta	aat	tta	cat	ttg	624
Gln	Leu	Pro 195	Leu	Leu	Ser	Leu	Tyr 200	Ala	Gln	Ala	Leu	Asn 205	Leu	His	Leu	
tta	tta	tta	aaa	gaa	gca	tct	ctt	ttt	gga	gaa	gga	ttt	gga	ttc	aca	672
Leu	Leu	Leu	Lys 210	Glu	Ala	Ser	Leu 215	Phe	Gly	Glu	Gly 220	Phe	Gly	Phe	Thr	
cag	ggg	gaa	att	tcc	aca	tat	tat	gaa	cgt	caa	ttg	gaa	cta	acc	gct	720
Gln	Gly	Glu	Ile	Ser	Thr 230	Tyr	Tyr	Glu	Arg	Gln 235	Leu	Glu	Leu	Thr	Ala 240	
aag	tac	act	aat	tac	tgt	gaa	act	ttt	tat	aat	aca	ggg	tta	gaa	cgt	768
Lys	Tyr	Thr	Asn 245	Tyr	Cys	Glu	Thr	Phe	Tyr 250	Asn	Thr	Gly	Leu	Glu	Arg 255	
tta	aga	gga	aca	aat	act	gaa	agt	ttt	tta	aga	tat	cat	caa	ttc	cgt	816
Leu	Arg	Gly	Thr 260	Asn	Thr	Glu	Ser	Phe 265	Leu	Arg	Tyr	His	Gln	Phe	Arg 270	
aga	gaa	atg	act	tta	tta	tta	tta	gaa	tta	tta	gcg	cta	ttt	cca	tat	864
Arg	Glu	Met 275	Thr	Leu	Leu	Leu	Leu 280	Glu	Leu	Leu	Ala	Leu	Phe	Pro	Tyr 285	
tat	gaa	tta	cga	ctt	tat	cca	acg	gga	tca	aac	cca	cag	ctt	aca	cgt	912
Tyr	Glu	Leu	Arg	Leu	Tyr	Pro 295	Thr	Gly	Ser	Asn	Pro 300	Gln	Leu	Thr	Arg	
gag	tta	tat	aca	gaa	ccg	att	tta	ttt	aat	cca	cca	gct	aat	tta	gga	960
Glu	Leu	Tyr	Thr	Glu	Pro 310	Ile	Leu	Phe	Asn	Pro 315	Pro	Ala	Asn	Leu	Gly 320	
ctt	tgc	cga	cgt	ttt	ggg	act	aat	ccc	tat	aat	act	ttt	tct	gag	ctc	1008
Leu	Cys	Arg	Arg	Phe 325	Gly	Thr	Asn	Pro	Tyr 330	Asn	Thr	Phe	Ser	Glu	Leu 335	
gaa	aat	gcc	ttc	att	cgc	cca	cca	cat	ctt	ttt	gaa	agg	ctg	aat	agc	1056
Glu	Asn	Ala	Phe 340	Ile	Arg	Pro	Pro	His 345	Leu	Phe	Glu	Arg	Leu	Asn	Ser 350	
tta	aca	atc	agc	agt	aat	cga	ttt	cca	tta	tca	tct	aat	ttt	atg	gaa	1104
Leu	Thr	Ile 355	Ser	Ser	Asn	Arg	Phe 360	Pro	Leu	Ser	Ser	Asn 365	Phe	Met	Glu	
tat	ttt	tca	gga	cat	acg	tta	cgc	cgt	agt	tat	ctg	aac	gaa	tca	gca	1152
Tyr	Phe	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Glu	Ser	Ala	

370	375	380	
tta caa gaa gaa agt tat ggc cta att aca acc aca aga gca aca att Leu Gln Glu Glu Ser Tyr Gly Leu Ile Thr Thr Thr Arg Ala Thr Ile 385 390 395 400			1200
aat ccc gga tta gaa gga aca aac cgc ata gag tca acg gca tta gaa Asn Pro Gly Leu Glu Gly Thr Asn Arg Ile Glu Ser Thr Ala Leu Glu 405 410 415			1248
ttt cgt tct gca ttg ata ggt ata tat ggc tta aat aga gct tct ttt Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Leu Asn Arg Ala Ser Phe 420 425 430			1296
tta cca gga ggc ttg ttt aat ggt acg act tct cct gct aat gga gga Leu Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly 435 440 445			1344
tgt aga gaa ctc tat gaa aca aat gaa gaa tta cca cca gaa gaa agt Cys Arg Glu Leu Tyr Glu Thr Asn Glu Glu Leu Pro Pro Glu Glu Ser 450 455 460			1392
acc gga agt tca acc cat aga cta tct cat tta acc ttt ttt agc ttt Thr Gly Ser Ser Thr His Arg Leu Ser His Leu Thr Phe Phe Ser Phe 465 470 475 480			1440
caa act aat cag gct gga tct ata gct aat gca gga agt tta cct act Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Leu Pro Thr 485 490 495			1488
tat tta ttt acc cgt cgt gaa tta gaa ctt aat aat acg att acc cca Tyr Leu Phe Thr Arg Arg Glu Leu Glu Leu Asn Asn Thr Ile Thr Pro 500 505 510			1536
aat aga att aca caa tta cca ttg tta aag gca tct gca cct tta tcg Asn Arg Ile Thr Gln Leu Pro Leu Leu Lys Ala Ser Ala Pro Leu Ser 515 520 525			1584
ggt act acg tta tta aaa ggt cca gga ttt aca gga ggg ggt ata ctc Gly Thr Thr Leu Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu 530 535 540			1632
cga aga aca act aat ggc aca ttt gga acg tta aga tta acg tta aat Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Leu Thr Leu Asn 545 550 555 560			1680
tca cca tta aca caa caa tat cgc cta aga tta cgt ttt gcc tca aca Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Leu Arg Phe Ala Ser Thr 565 570 575			1728
gga aat ttc agt ata agg tta ctc cgt gga ggg tta tct atc ggt gaa Gly Asn Phe Ser Ile Arg Leu Leu Arg Gly Gly Leu Ser Ile Gly Glu 580 585 590			1776
tta aga tta ggg agc aca atg aac aga ggg cag gaa cta act tac gaa Leu Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu 595 600 605			1824

tcc	ttt	ttc	aca	aga	gag	ttt	act	act	act	ggt	ccg	ttc	aat	ccg	cct	1872
Ser	Phe	Phe	Thr	Arg	Glu	Phe	Thr	Thr	Thr	Gly	Pro	Phe	Asn	Pro	Pro	
610						615					620					

ttt	aca	ttt	aca	caa	gct	caa	gag	att	cta	aca	tta	aat	gca	gaa	ggt	1920
Phe	Thr	Phe	Thr	Gln	Ala	Gln	Glu	Ile	Leu	Thr	Leu	Asn	Ala	Glu	Gly	
625					630					635					640	

tta	agc	acc	ggt	ggt	gaa	tat	tat	ata	gaa	aga	att	gaa	att	tta	cct	1968
Leu	Ser	Thr	Gly	Gly	Glu	Tyr	Tyr	Ile	Glu	Arg	Ile	Glu	Ile	Leu	Pro	
				645					650					655		

tta	aat	ccg	gca	cga	gaa	gcg	gaa	gag	gaa	tta	gaa	gcg	gcg	aag	aaa	2016
Leu	Asn	Pro	Ala	Arg	Glu	Ala	Glu	Glu	Glu	Leu	Glu	Ala	Ala	Lys	Lys	
			660					665					670			

gcg																2019
Ala																

<210> 10
 <211> 673
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Artificial sequence description: Cry9Ca1-100%

<400> 10
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 1 5 10 15
 Cys Gly Cys Pro Ser Glu Glu Glu Leu Arg Tyr Pro Leu Ala Ser Glu
 20 25 30
 Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Glu Tyr Leu Gln Met
 35 40 45
 Thr Glu Glu Glu Tyr Thr Glu Ser Tyr Ile Asn Pro Ser Leu Ser Ile
 50 55 60
 Ser Gly Arg Glu Ala Leu Gln Thr Ala Leu Thr Val Ile Arg Arg Ile
 65 70 75 80
 Leu Gly Ala Leu Gly Leu Pro Phe Ser Gly Gln Ile Leu Ser Phe Tyr
 85 90 95
 Gln Phe Leu Leu Asn Thr Leu Phe Pro Leu Asn Glu Thr Ala Ile Phe
 100 105 110
 Glu Ala Phe Met Arg Gln Leu Glu Glu Leu Leu Asn Gln Gln Ile Thr
 115 120 125
 Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Glu
 130 135 140

Ser	Phe	Asn	Leu	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Phe	Leu	Ala	Glu	Arg	145	150	155	160
Asn	Glu	Thr	Arg	Asn	Leu	Ser	Leu	Leu	Arg	Ala	Gln	Phe	Ile	Ala	Leu	165	170	175	
Glu	Leu	Glu	Phe	Leu	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Leu	Asn	Gly	Gln	180	185	190	
Gln	Leu	Pro	Leu	Leu	Ser	Leu	Tyr	Ala	Gln	Ala	Leu	Asn	Leu	His	Leu	195	200	205	
Leu	Leu	Leu	Lys	Glu	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Phe	Gly	Phe	Thr	210	215	220	
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Glu	Arg	Gln	Leu	Glu	Leu	Thr	Ala	225	230	235	240
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Phe	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	245	250	255	
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Phe	Leu	Arg	Tyr	His	Gln	Phe	Arg	260	265	270	
Arg	Glu	Met	Thr	Leu	Leu	Leu	Leu	Glu	Leu	Leu	Ala	Leu	Phe	Pro	Tyr	275	280	285	
Tyr	Glu	Leu	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg	290	295	300	
Glu	Leu	Tyr	Thr	Glu	Pro	Ile	Leu	Phe	Asn	Pro	Pro	Ala	Asn	Leu	Gly	305	310	315	320
Leu	Cys	Arg	Arg	Phe	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu	325	330	335	
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Glu	Arg	Leu	Asn	Ser	340	345	350	
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Leu	Ser	Ser	Asn	Phe	Met	Glu	355	360	365	
Tyr	Phe	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Glu	Ser	Ala	370	375	380	
Leu	Gln	Glu	Glu	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile	385	390	395	400
Asn	Pro	Gly	Leu	Glu	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Leu	Glu	405	410	415	
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Leu	Asn	Arg	Ala	Ser	Phe	420	425	430	
Leu	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly	435	440	445	

Cys Arg Glu Leu Tyr Glu Thr Asn Glu Glu Leu Pro Pro Glu Glu Ser
 450 455 460
 Thr Gly Ser Ser Thr His Arg Leu Ser His Leu Thr Phe Phe Ser Phe
 465 470 475 480
 Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Leu Pro Thr
 485 490 495
 Tyr Leu Phe Thr Arg Arg Glu Leu Glu Leu Asn Asn Thr Ile Thr Pro
 500 505 510
 Asn Arg Ile Thr Gln Leu Pro Leu Leu Lys Ala Ser Ala Pro Leu Ser
 515 520 525
 Gly Thr Thr Leu Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu
 530 535 540
 Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Leu Thr Leu Asn
 545 550 555 560
 Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Leu Arg Phe Ala Ser Thr
 565 570 575
 Gly Asn Phe Ser Ile Arg Leu Leu Arg Gly Gly Leu Ser Ile Gly Glu
 580 585 590
 Leu Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu
 595 600 605
 Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro
 610 615 620
 Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Leu Asn Ala Glu Gly
 625 630 635 640
 Leu Ser Thr Gly Gly Glu Tyr Tyr Ile Glu Arg Ile Glu Ile Leu Pro
 645 650 655
 Leu Asn Pro Ala Arg Glu Ala Glu Glu Glu Leu Glu Ala Ala Lys Lys
 660 665 670

Ala

<210> 11
 <211> 2019
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description: Cry9Ca1-25%

<220>
 <221> CDS

<222> (1) .. (2019)

<400> 11

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Met	Asn	Arg	Asn	Asn	Gln	Asn	Glu	Tyr	Glu	Ile	Ile	Asp	Ala	Pro	His	
1				5				10					15			
tgt	ggg	tgt	cca	tca	gat	gac	gat	gtg	agg	tat	cct	ttg	gca	agt	gac	96
Cys	Gly	Cys	Pro	Ser	Asp	Asp	Asp	Val	Arg	Tyr	Pro	Leu	Ala	Ser	Asp	
			20					25					30			
cca	aat	gca	gcg	tta	caa	aat	atg	aac	tat	aaa	gat	tac	tta	caa	atg	144
Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met	
		35					40					45				
aca	gat	gag	gac	tac	act	gat	tct	tat	ata	aat	cct	agt	tta	tct	att	192
Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile	
	50					55					60					
agt	ggg	aga	gaa	gca	tta	cag	act	gag	ctt	acg	tta	tta	ggg	aga	ata	240
Ser	Gly	Arg	Glu	Ala	Leu	Gln	Thr	Ala	Leu	Thr	Leu	Leu	Gly	Arg	Ile	
65					70					75					80	
ctc	ggg	gct	tta	ggg	gtt	ccg	ttt	tct	gga	caa	ata	tta	agt	ttt	tat	288
Leu	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ser	Gly	Gln	Ile	Leu	Ser	Phe	Tyr	
				85					90					95		
caa	ttc	ctt	tta	aat	aca	ctg	tgg	cca	gtt	aat	gat	aca	gct	ata	tgg	336
Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp	
			100					105					110			
gaa	gct	ttc	atg	cga	cag	gtg	gag	gaa	ctt	gtc	aat	caa	caa	ata	aca	384
Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr	
		115					120					125				
gaa	ttt	gca	aga	aat	cag	gca	ctt	gca	aga	ttg	caa	gga	tta	gga	gaa	432
Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Glu	
	130					135					140					
tct	ttt	aat	gta	tat	caa	cgt	tcc	ctt	caa	aat	tgg	ttg	gct	gat	cga	480
Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg	
145					150					155					160	
aat	gat	aca	cga	aat	tta	agt	tta	tta	cgt	gct	caa	ttt	ata	gct	tta	528
Asn	Asp	Thr	Arg	Asn	Leu	Ser	Leu	Leu	Arg	Ala	Gln	Phe	Ile	Ala	Leu	
				165					170					175		
gac	ctt	gat	ttt	gtt	aat	gct	att	cca	ttg	ttt	gca	gta	aat	gga	cag	576
Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln	
			180					185					190			
cag	gtt	cca	tta	ctg	tca	gta	tat	gca	caa	gct	tta	aat	tta	cat	ttg	624
Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Leu	Asn	Leu	His	Leu	
		195					200					205				
tta	tta	tta	aaa	gaa	gca	tct	ctt	ttt	gga	gaa	gga	tgg	gga	ttc	aca	672
Leu	Leu	Leu	Lys	Glu	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr	

210	215	220	
cag ggg gaa att tcc aca tat tat gaa cgt caa ttg gaa cta acc gct Gln Gly Glu Ile Ser Thr Tyr Tyr Glu Arg Gln Leu Glu Leu Thr Ala 225 230 235 240			720
aag tac act aat tac tgt gaa act tgg tat aat aca ggt tta gaa cgt Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu Glu Arg 245 250 255			768
tta aga gga aca aat act gaa agt ttt tta aga tat cat caa ttc cgt Leu Arg Gly Thr Asn Thr Glu Ser Phe Leu Arg Tyr His Gln Phe Arg 260 265 270			816
aga gaa atg act tta gtg gta tta gat gtt gtg gcg cta ttt cca tat Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe Pro Tyr 275 280 285			864
tat gat gta cga ctt tat cca acg gga tca aac cca cag ctt aca cgt Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg 290 295 300			912
gag gta tat aca gat ccg att gta ttt aat cca cca gct aat tta gga Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn Leu Gly 305 310 315 320			960
ctt tgc cga cgt tgg ggt act aat ccc tat aat act ttt tct gag ctc Leu Cys Arg Arg Trp Gly Thr Asn Pro Tyr Asn Thr Phe Ser Glu Leu 325 330 335			1008
gaa aat gcc ttc att cgc cca cca cat ctt ttt gaa agg ctg aat agc Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Glu Arg Leu Asn Ser 340 345 350			1056
tta aca atc agc agt aat cga ttt cca gtt tca tct aat ttt atg gaa Leu Thr Ile Ser Ser Asn Arg Phe Pro Val Ser Ser Asn Phe Met Glu 355 360 365			1104
tat ttt tca gga cat acg tta cgc cgt agt tat ctg aac gat tca gca Tyr Phe Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Asp Ser Ala 370 375 380			1152
gta caa gaa gat agt tat ggc cta att aca acc aca aga gca aca att Val Gln Glu Asp Ser Tyr Gly Leu Ile Thr Thr Thr Arg Ala Thr Ile 385 390 395 400			1200
aat ccc gga gtt gat gga aca aac cgc ata gag tca acg gca gta gat Asn Pro Gly Val Asp Gly Thr Asn Arg Ile Glu Ser Thr Ala Val Asp 405 410 415			1248
ttt cgt tct gca ttg ata ggt ata tat ggc gtg aat aga gct tct ttt Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Val Asn Arg Ala Ser Phe 420 425 430			1296
gtc cca gga ggc ttg ttt aat ggt acg act tct cct gct aat gga gga Val Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly 435 440 445			1344

tgt	aga	gat	ctc	tat	gat	aca	aat	gat	gaa	tta	cca	cca	gat	gaa	agt	1392
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser	
	450					455					460					
acc	gga	agt	tca	acc	cat	aga	cta	tct	cat	tta	acc	ttt	ttt	agc	ttt	1440
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Leu	Thr	Phe	Phe	Ser	Phe	
465					470					475					480	
caa	act	aat	cag	gct	gga	tct	ata	gct	aat	gca	gga	agt	gta	cct	act	1488
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr	
				485					490					495		
tat	gtt	tgg	acc	cgt	cgt	gat	gtg	gac	ctt	aat	aat	acg	att	acc	cca	1536
Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	Thr	Pro	
			500					505					510			
aat	aga	att	aca	caa	tta	cca	ttg	gta	aag	gca	tct	gca	cct	gtt	tcg	1584
Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro	Val	Ser	
		515					520					525				
ggg	act	acg	gtc	tta	aaa	ggg	cca	gga	ttt	aca	gga	ggg	ggg	ata	ctc	1632
Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	Ile	Leu	
	530					535					540					
cga	aga	aca	act	aat	ggc	aca	ttt	gga	acg	tta	aga	gta	acg	gtt	aat	1680
Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr	Val	Asn	
545					550					555					560	
tca	cca	tta	aca	caa	caa	tat	cgc	cta	aga	tta	cgt	ttt	gcc	tca	aca	1728
Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Leu	Arg	Phe	Ala	Ser	Thr	
				565				570						575		
gga	aat	ttc	agt	ata	agg	gta	ctc	cgt	gga	ggg	gtt	tct	atc	ggg	gat	1776
Gly	Asn	Phe	Ser	Ile	Arg	Val	Leu	Arg	Gly	Gly	Val	Ser	Ile	Gly	Asp	
			580					585					590			
gtt	aga	tta	ggg	agc	aca	atg	aac	aga	ggg	cag	gaa	cta	act	tac	gaa	1824
Val	Arg	Leu	Gly	Ser	Thr	Met	Asn	Arg	Gly	Gln	Glu	Leu	Thr	Tyr	Glu	
		595					600					605				
tcc	ttt	ttc	aca	aga	gag	ttt	act	act	act	ggg	ccg	ttc	aat	ccg	cct	1872
Ser	Phe	Phe	Thr	Arg	Glu	Phe	Thr	Thr	Thr	Gly	Pro	Phe	Asn	Pro	Pro	
	610					615					620					
ttt	aca	ttt	aca	caa	gct	caa	gag	att	cta	aca	gtg	aat	gca	gaa	ggg	1920
Phe	Thr	Phe	Thr	Gln	Ala	Gln	Glu	Ile	Leu	Thr	Val	Asn	Ala	Glu	Gly	
625					630					635					640	
gtt	agc	acc	ggg	ggg	gaa	tat	tat	ata	gat	aga	att	gaa	att	gtc	cct	1968
Val	Ser	Thr	Gly	Gly	Glu	Tyr	Tyr	Ile	Asp	Arg	Ile	Glu	Ile	Val	Pro	
				645					650					655		
gtg	aat	ccg	gca	cga	gaa	gag	gaa	gag	gat	tta	gaa	gag	gag	aag	aaa	2016
Val	Asn	Pro	Ala	Arg	Glu	Ala	Glu	Glu	Asp	Leu	Glu	Ala	Ala	Lys	Lys	
			660					665					670			

gcg
Ala

2019

<210> 12
<211> 673
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial sequence description: Cry9Ca1-25%

<400> 12

Met	Asn	Arg	Asn	Asn	Gln	Asn	Glu	Tyr	Glu	Ile	Ile	Asp	Ala	Pro	His
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Cys	Gly	Cys	Pro	Ser	Asp	Asp	Asp	Val	Arg	Tyr	Pro	Leu	Ala	Ser	Asp
			20					25					30		

Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met
		35					40					45			

Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile
	50					55					60				

Ser	Gly	Arg	Glu	Ala	Leu	Gln	Thr	Ala	Leu	Thr	Leu	Leu	Gly	Arg	Ile
65					70					75					80

Leu	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ser	Gly	Gln	Ile	Leu	Ser	Phe	Tyr
				85					90					95	

Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp
			100					105					110		

Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr
		115					120					125			

Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Glu
	130					135					140				

Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg
145					150					155					160

Asn	Asp	Thr	Arg	Asn	Leu	Ser	Leu	Leu	Arg	Ala	Gln	Phe	Ile	Ala	Leu
				165					170					175	

Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln
			180					185					190		

Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Leu	Asn	Leu	His	Leu
		195					200					205			

Leu	Leu	Leu	Lys	Glu	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr
	210					215					220				

Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Glu	Arg	Gln	Leu	Glu	Leu	Thr	Ala
225					230					235					240

Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	
			245						250					255		
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Phe	Leu	Arg	Tyr	His	Gln	Phe	Arg	
			260					265					270			
Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr	
		275					280					285				
Tyr	Asp	Val	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg	
	290					295					300					
Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Leu	Gly	
305					310					315					320	
Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu	
				325					330					335		
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Glu	Arg	Leu	Asn	Ser	
			340					345					350			
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Glu	
		355					360					365				
Tyr	Phe	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala	
	370					375					380					
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile	
385					390					395					400	
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp	
				405					410					415		
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe	
			420					425					430			
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly	
		435					440					445				
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser	
	450					455					460					
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Leu	Thr	Phe	Phe	Ser	Phe	
465					470					475					480	
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr	
				485					490					495		
Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	Thr	Pro	
			500					505					510			
Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro	Val	Ser	
		515					520					525				
Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	Ile	Leu	
	530					535					540					

Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr	Val	Asn
545					550					555					560
Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Leu	Arg	Phe	Ala	Ser	Thr
				565					570					575	
Gly	Asn	Phe	Ser	Ile	Arg	Val	Leu	Arg	Gly	Gly	Val	Ser	Ile	Gly	Asp
			580					585					590		
Val	Arg	Leu	Gly	Ser	Thr	Met	Asn	Arg	Gly	Gln	Glu	Leu	Thr	Tyr	Glu
		595					600					605			
Ser	Phe	Phe	Thr	Arg	Glu	Phe	Thr	Thr	Thr	Gly	Pro	Phe	Asn	Pro	Pro
	610					615					620				
Phe	Thr	Phe	Thr	Gln	Ala	Gln	Glu	Ile	Leu	Thr	Val	Asn	Ala	Glu	Gly
625				630						635					640
Val	Ser	Thr	Gly	Gly	Glu	Tyr	Tyr	Ile	Asp	Arg	Ile	Glu	Ile	Val	Pro
			645						650					655	
Val	Asn	Pro	Ala	Arg	Glu	Ala	Glu	Glu	Asp	Leu	Glu	Ala	Ala	Lys	Lys
		660						665					670		

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<210> 14
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<400> 14
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<210> 15
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<223> Artificial sequence description: mutant 3

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gaattattag aattttttatt attaagtgtt

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<210> 16

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<223> Artificial sequence description: mutant 4

<400> 16

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<210> 18

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<223> Artificial sequence description: mutant 6

<400> 18

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30

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<223> Artificial sequence description: mutant 7

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gaacgattag aattattatt attaagtgtt

30

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<400> 29

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24

<210> 30

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<400> 30

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24

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<223> Artificial sequence description: mutant 19

<400> 31

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24

<210> 32

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<223> Artificial sequence description: mutant 20

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24

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<223> Artificial sequence description: mutant 21

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24

<210> 34

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<223> Artificial sequence description: mutant 22

<400> 34

ttattagaat taaat

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<211> 15

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<223> Artificial sequence description: mutant 23

<400> 35

ttattatttt taaat

15

<210> 36

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<223> Artificial sequence description: mutant 24

<400> 36

ttagaattat taaat

15

<210> 37

<211> 15

<212> DNA

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<223> Artificial sequence description: mutant 25

<400> 37

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<210> 38

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<400> 38

ttagaagaat taaat

15

<210> 39
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<400> 39
ttagaat ttt taaat 15

<210> 40
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<400> 40
ttagaat tttg aaaat 15

<210> 41
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<400> 41
ttagaagaag aaaat 15

<210> 42
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<210> 45
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oligonucleotide 4

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cgaaatgata cacgattatt aagtgttggtt cgt 33

<210> 46
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oligonucleotide 5

<400> 46
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<210> 47
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oligonucleotide 6

<400> 47
ttggctgata gaaatgaatt tttaaattta agtgttggtt 39

<210> 48
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ttggctgatc gaaatgaatt tttattatta agtggttggt

39

<210> 49
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39

<210> 50
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39

<210> 51
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39

<210> 52
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39

<210> 53

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caaaattggt tggctgaatt aaatgaatta ttaa

36

<210> 54

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36

<210> 55

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39

<210> 56

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<223> Artificial sequence description:
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39

<210> 57

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<223> Artificial sequence description:
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<400> 57

caaaattggt tggctgaatt attagaagaa ttattatta

39

<210> 58

<211> 39

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<223> Artificial sequence description:
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<400> 58

caaaattggt tggctgaacg attagaattt ttattatta

39

<210> 59

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<223> Artificial sequence description:
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<400> 59

caaaattggt tggctgaacg attagaatta ttattatta

39

<210> 60

<211> 39

<212> DNA

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caaaattggt tggctgaatt agaagaatta ttattatta

39

<210> 61

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 <210> 62
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 <210> 64
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 <210> 65
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oligonucleotide 24

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ttattaaatg gacagcagtt tccattactg tcagta

36

<210> 66

<211> 36

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ttattaaatg gacagcagga accattactg tcagta

36

<210> 67

<211> 36

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gaagaaaatg gacagcagtt accattactg tcagta

36

<210> 68

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36

<210> 69

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45

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<210> 72
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<210> 74
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<223> Artificial sequence description:
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45

<210> 75

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<400> 75

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45

<210> 76

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oligonucleotide 35

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gatgcatctc tttttttaga aggatgggga ttc

33

<210> 77

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36

<210> 78

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<210> 81
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<210> 82
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<210> 83

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45

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45

<210> 85
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45

<210> 86
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oligonucleotide 45

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39

<210> 87
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39

<210> 88

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oligonucleotide 47

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39

<210> 89

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39

<210> 90

<211> 39

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39

<210> 91

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39

<210> 92
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<210> 93
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ggtttagatc gtttagaaga agaaaatact gaaagttgg 39

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oligonucleotide 53

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tgaatatgaa attattgaag cccccattg 30

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oligonucleotide 54

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27

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gaactataaa gaatacttac aaatg

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26

<210> 99

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<210> 100

<211> 36

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<210> 101
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oligonucleotide 60

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oligonucleotide 61

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oligonucleotide 62

<400> 103
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oligonucleotide 63

<400> 104
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oligonucleotide 64

<400> 105
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24

<210> 106
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26

<210> 107
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oligonucleotide 66

<400> 107
gaggaacttt taaatcaaca aataac

26

<210> 108
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oligonucleotide 67

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21

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oligonucleotide 68

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23

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oligonucleotide 69

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21

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oligonucleotide 70

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17

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23

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<223> Artificial sequence description:
oligonucleotide 72

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<223> Artificial sequence description:
oligonucleotide 73

<400> 114
gctcaattta tagctttaga acttgaattt ttaaattgcta ttccattg 48

<210> 115
<211> 27
<212> DNA
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<220>
<223> Artificial sequence description:
oligonucleotide 74

<400> 115
ccattgtttg cattaaatgg acagcag 27

<210> 116
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 75

<400> 116
ccattgtttg cattaaatgg acagcag 27

<210> 117
<211> 27
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<220>
<223> Artificial sequence description:
oligonucleotide 76

<400> 117
ccattactgt cattatatgc acaagct 27

<210> 118
<211> 27

<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 77

<400> 118
tatgcacaag ctttaaattt acatttg

27

<210> 119
<211> 23
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<220>
<223> Artificial sequence description:
oligonucleotide 78

<400> 119
ttattaaaag aagcatctct ttt

23

<210> 120
<211> 25
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<220>
<223> Artificial sequence description:
oligonucleotide 79

<400> 120
tggagaagga tttggattca cacag

25

<210> 121
<211> 24
<212> DNA
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<220>
<223> Artificial sequence description:
oligonucleotide 80

<400> 121
cacatattat gaacgtcaat tgga

24

<210> 122
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:

oligonucleotide 81

<400> 122

tactgtgaaa ctttttataa tacagggt

28

<210> 123

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 82

<400> 123

tacaggttta gaacgttta gagga

25

<210> 124

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 83

<400> 124

aatactgaaa gttttttaag atatcatc

28

<210> 125

<211> 51

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 84

<400> 125

gtagagaaat gactttatta ttattagaat tattagcgct atttccatat t

51

<210> 126

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 85

<400> 126

atattatgaa ttacgacttt atccaac

27

<210> 127
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 86

<400> 127
cttacacgtg agttatatac aga

23

<210> 128
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 87

<400> 128
tatacagaac cgatttttatt taatccacc

29

<210> 129
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 88

<400> 129
ccaccagcta atttaggact ttgccgac

28

<210> 130
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 89

<400> 130
ctttgccgac gtttttggtac taatccc

27

<210> 131
<211> 23
<212> DNA
<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 90

<400> 131

catctttttg aaaggctgaa tag

23

<210> 132

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 91

<400> 132

taatcgattt ccattatcat ctaattttat

30

<210> 133

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 92

<400> 133

ctaattttat ggaatatttt tcaggacata cgttac

36

<210> 134

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 93

<400> 134

tagttatctg aacgaatcag cattacaaga aga

33

<210> 135

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 94

<400> 135
caagaagaaa gttatggcct 20

<210> 136
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 95

<400> 136
caattaatcc cggattagaa ggaacaaacc gcata 35

<210> 137
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 96

<400> 137
gagtcaacgg cattagaatt tcgttctgca 30

<210> 138
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 97

<400> 138
ggtatatatg gcttaaatag agcttc 26

<210> 139
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 98

<400> 139
tagagcttct tttttaccag gaggcttggt 30

<210> 140

<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 99

<400> 140
ctgctaattgg aggatgtaga gaactctatg a

31

<210> 141
<211> 17
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 100

<400> 141
ctctatgaaa caaatga

17

<210> 142
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 101

<400> 142
acaaatgaag aattaccacc

20

<210> 143
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 102

<400> 143
attaccacca gaagaaagta ccggaag

27

<210> 144
<211> 30
<212> DNA
<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 103

<400> 144
agactatctc atttaacctt ttttagcttt

30

<210> 145
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 104

<400> 145
gctaatagcag gaagtttacc tacttat

27

<210> 146
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 105

<400> 146
cctacttatt tatattaccg tcgtga

26

<210> 147
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 106

<400> 147
accgcgtcgtg aattagaact taataatcg att

33

<210> 148
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 107

<400> 148
attaccattg ttaaaggcat ctgc

24

<210> 149
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 108

<400> 149
aaggcatctg cacctttatc gggactacg 30

<210> 150
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 109

<400> 150
tcgggtacta cggtattaaa aggtccagg 29

<210> 151
<211> 40
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 110

<400> 151
acatttggaa cgtaagatt aacgttaaatt tcaccattaa 40

<210> 152
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 111

<400> 152
cacaacaata tcgcctaaga ttacgttttg cctcaac 37

<210> 153
<211> 31
<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 112

<400> 153

aaatttcagt ataaggttac tccgtggagg g

31

<210> 154

<211> 35

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 113

<400> 154

ataagggtac tccgtggagg gttatctatc ggtga

35

<210> 155

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 114

<400> 155

tctatcggtg aattaagatt agggagcac

29

<210> 156

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 115

<400> 156

caagagattc taacattaaa tgcagaaggt

30

<210> 157

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 116

<400> 157
aatgcagaag gtttaagcac cggcggcgtaa ta

32

<210> 158
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 117

<400> 158
gtggcgaata ttatatagaa agaattgaaa tt

32

<210> 159
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 118

<400> 159
agaattgaaa ttttaccttt aaatccggca cgagaag

37

<210> 160
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 119

<400> 160
cgagaagcgg aagaggaatt agaagcggcg

30